

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/524,971
Source: PT/10
Date Processed by STIC: 2/26/05

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PCT

RAW SEQUENCE LISTING

DATE: 02/26/2005

PATENT APPLICATION: US/10/524,971

TIME: 10:36:14

Input Set : A:\Sequence list-13173-00003-US.txt

Output Set: N:\CRF4\02262005\J524971.raw

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3 <110> APPLICANT: Klebsattel, Martin
4      Sauer, Matt
5      Flachmann, Ralf
6      Schopfer, Christel Renate
8 <120> TITLE OF INVENTION: Process for the preparation of beta-carotenoids
10 <130> FILE REFERENCE: 13173-00003-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/524,971
C--> 12 <141> CURRENT FILING DATE: 2005-02-18
12 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/009101
13 <151> PRIOR FILING DATE: 2003-08-18
15 <150> PRIOR APPLICATION NUMBER: DE 102 38 980.2
16 <151> PRIOR FILING DATE: 2002-08-20
18 <150> PRIOR APPLICATION NUMBER: DE 102 38 979.9
19 <151> PRIOR FILING DATE: 2002-08-20
21 <150> PRIOR APPLICATION NUMBER: DE 102 58 971.2
22 <151> PRIOR FILING DATE: 2002-12-16
24 <160> NUMBER OF SEQ ID NOS: 51
26 <170> SOFTWARE: PatentIn version 3.3
30 <210> SEQ ID NO: 1
32 <211> LENGTH: 1666
34 <212> TYPE: DNA
36 <213> ORGANISM: Lycopersicon esculentum
38 <220> FEATURE:
40 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)..(1494)
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46 Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
47 1          5          10          15
49 aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc      96
50 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
51          20          25          30
53 acc acc aaa aaa aaa tca aga aaa tgt ctt ctt aga aac aaa agt agt      144
54 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
55          35          40          45
57 aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag      192
58 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
59          50          55          60
61 tct tta gat gtt aac atc tca tgg gtt gat cct aat tcg aat cgg gct      240
62 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
63 65          70          75          80
65 caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta      288
66 Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu

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| | | | | |
|---|-----|-----|-----|------|
| 67 | 85 | 90 | 95 | |
| 69 gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct | | | | 336 |
| 70 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro | | | | |
| 71 | 100 | 105 | 110 | |
| 73 tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag | | | | 384 |
| 74 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu | | | | |
| 75 | 115 | 120 | 125 | |
| 77 ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg | | | | 432 |
| 78 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met | | | | |
| 79 | 130 | 135 | 140 | |
| 81 act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca | | | | 480 |
| 82 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro | | | | |
| 83 145 | 150 | 155 | 160 | |
| 85 tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt | | | | 528 |
| 86 Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser | | | | |
| 87 | 165 | 170 | 175 | |
| 89 tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg | | | | 576 |
| 90 Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val | | | | |
| 91 | 180 | 185 | 190 | |
| 93 gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag | | | | 624 |
| 94 Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys | | | | |
| 95 | 195 | 200 | 205 | |
| 97 ata aga ggt agt ttg gtt gtg gat gca agt ggt ttt gct agt gat ttt | | | | 672 |
| 98 Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe | | | | |
| 99 | 210 | 215 | 220 | |
| 101 ata gag tat gac agg cca aga aac cat ggt tat caa att gct cat ggg | | | | 720 |
| 102 Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly | | | | |
| 103 225 | 230 | 235 | 240 | |
| 105 gtt tta gta gaa gtt gat aat cat cca ttt gat ttg gat aaa atg gtg | | | | 768 |
| 106 Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val | | | | |
| 107 | 245 | 250 | 255 | |
| 109 ctt atg gat tgg agg gat tct cat ttg ggt aat gag cca tat tta agg | | | | 816 |
| 110 Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg | | | | |
| 111 | 260 | 265 | 270 | |
| 113 gtg aat aat gct aaa gaa cca aca ttc ttg tat gca atg cca ttt gat | | | | 864 |
| 114 Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp | | | | |
| 115 | 275 | 280 | 285 | |
| 117 aga gat ttg gtt ttc ttg gaa gag act tct ttg gtg agt cgt cct gtt | | | | 912 |
| 118 Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val | | | | |
| 119 | 290 | 295 | 300 | |
| 121 tta tcg tat atg gaa gta aaa aga agg atg gtg gca aga tta agg cat | | | | 960 |
| 122 Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His | | | | |
| 123 305 | 310 | 315 | 320 | |
| 125 ttg ggg atc aaa gtg aaa agt gtt att gag gaa gag aaa tgt gtg atc | | | | 1008 |
| 126 Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile | | | | |
| 127 | 325 | 330 | 335 | |
| 129 cct atg gga gga cca ctt ccg cgg att cct caa aat gtt atg gct att | | | | 1056 |
| 130 Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile | | | | |
| 131 | 340 | 345 | 350 | |

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133 ggt ggg aat tca ggg ata gtt cat cca tca aca ggg tac atg gtg gct      1104
134 Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
135      355      360      365
137 agg agc atg gct tta gca cca gta cta gct gaa gcc atc gtc gag ggg      1152
138 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly
139      370      375      380
141 ctt ggc tca aca aga atg ata aga ggg tct caa ctt tac cat aga gtt      1200
142 Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val
143 385      390      395      400
145 tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat      1248
146 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr
147      405      410      415
149 tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg      1296
150 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
151      420      425      430
153 aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg      1344
154 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
155      435      440      445
157 ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg      1392
158 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
159      450      455      460
161 tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca      1440
162 Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
163 465      470      475      480
165 aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag      1488
166 Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu
167      485      490      495
169 agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat      1544
170 Ser Leu
172 tttcatattt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact      1604
174 actattggaa agttaaaata tgtgtttggt gtatgttatt ctaatggaat ggattttgta      1664
176 aa      1666
179 <210> SEQ ID NO: 2
181 <211> LENGTH: 498
183 <212> TYPE: PRT
185 <213> ORGANISM: Lycopersicon esculentum
187 <400> SEQUENCE: 2
189 Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
190 1      5      10      15
193 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
194      20      25      30
197 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
198      35      40      45
201 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
202      50      55      60
205 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
206 65      70      75      80
209 Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
210      85      90      95

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213 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
214      100      105      110
217 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
218      115      120      125
221 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
222      130      135      140
225 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro
226 145      150      155      160
229 Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Asn Ser
230      165      170      175
233 Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val
234      180      185      190
237 Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys
238      195      200      205
241 Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe
242      210      215      220
245 Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly
246 225      230      235      240
249 Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val
250      245      250      255
253 Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg
254      260      265      270
257 Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp
258      275      280      285
261 Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val
262      290      295      300
265 Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His
266 305      310      315      320
269 Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Lys Cys Val Ile
270      325      330      335
273 Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile
274      340      345      350
277 Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
278      355      360      365
281 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly
282      370      375      380
285 Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val
286 385      390      395      400
289 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr
290      405      410      415
293 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
294      420      425      430
297 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
298      435      440      445
301 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
302      450      455      460
305 Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
306 465      470      475      480
309 Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu

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310                               485                               490                               495
313 Ser Leu
317 <210> SEQ ID NO: 3
319 <211> LENGTH: 1608
321 <212> TYPE: DNA
323 <213> ORGANISM: Haematococcus pluvialis
325 <220> FEATURE:
327 <221> NAME/KEY: CDS
329 <222> LOCATION: (3)..(971)
331 <400> SEQUENCE: 3
332 ct aca ttt cac aag ccc gtg agc ggt gca agc gct ctg ccc cac atc      47
333   Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
334     1             5             10             15
336 ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg      95
337 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
338             20             25             30
340 tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc      143
341 Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala
342             35             40             45
344 cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg      191
345 Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser
346     50             55             60
348 tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga      239
349 Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly
350     65             70             75
353 acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca      287
354 Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala
355 80             85             90             95
357 ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa      335
358 Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys
359             100            105            110
361 cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc      383
362 Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly
363             115            120            125
365 gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac      431
366 Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His
367             130            135            140
369 atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc      479
370 Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu
371             145            150            155
373 ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat      527
374 Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr
375 160             165             170             175
377 gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac      575
378 Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His
379             180            185            190
381 aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg      623
382 Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu
383             195            200            205

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date